Re-run

PCT

RAW SEQUENCE LISTING   DATE: 08/31/2001
PATENT APPLICATION: **US/09/674,035**   TIME: 11:38:07

Input Set : **A:\227274078.ST25.txt**
Output Set: **N:\CRF3\08312001\I674035.raw**

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 5 <120> TITLE OF INVENTION: Detecting the Expression of the DESC1 Gene in Squamous Cell
Carcinoma
 7 <130> FILE REFERENCE: 22727/04078
 9 <140> CURRENT APPLICATION NUMBER: 09/674,035
10 <141> CURRENT FILING DATE: 1999-11-11
12 <150> PRIOR APPLICATION NUMBER: PCT/IB99/01818
13 <151> PRIOR FILING DATE: 1999-11-11
15 <160> NUMBER OF SEQ ID NOS: 10
17 <170> SOFTWARE: PatentIn version 3.0
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21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
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35              20                  25                  30
37 gtg tgc att gga ctc act gtt cat tat gtg aga tat aat caa aag aag        144
38 Val Cys Ile Gly Leu Thr Val His Tyr Val Arg Tyr Asn Gln Lys Lys
39          35                  40                  45
41 acc tac aat tac tat agc aca ttg tca ttt aca act gac aaa cta tat        192
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43      50                  55                  60
45 gct gag ttt ggc aga gag gct tct aac aat ttt aca gaa atg agc cag        240
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53 gaa gaa ttt gtc aag tct cag gtt atc aag ttc agt caa gac aag cat        336
54 Glu Glu Phe Val Lys Ser Gln Val Ile Lys Phe Ser Gln Asp Lys His
55              100                 105                 110
57 gga gtg ttg gct cat atg ctg ttg att tgt aga ttt cac tct act gag        384
58 Gly Val Leu Ala His Met Leu Leu Ile Cys Arg Phe His Ser Thr Glu
59          115                 120                 125
61 gat cct gaa act gta gat aaa att gtt caa ctt gtt tta cat gaa aag        432
62 Asp Pro Glu Thr Val Asp Lys Ile Val Gln Leu Val Leu His Glu Lys
63      130                 135                 140
65 ctg caa gat gct gta gga ccc cct aaa gta gat cct cac tca gtt aaa        480
66 Leu Gln Asp Ala Val Gly Pro Pro Lys Val Asp Pro His Ser Val Lys
67 145                 150                 155                 160
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Input Set : A:\227274078.ST25.txt
Output Set: N:\CRF3\08312001\I674035.raw

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74  Cys Gly Thr Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val
75              180                 185                 190
77  ggt ggg aca gaa gta gaa gag ggt gaa tgg ccc tgg cag gct agc ctg        624
78  Gly Gly Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu
79              195                 200                 205
81  cag tgg gat ggg agt cat gcg tgt gga gca acc tta att aat gcc aca        672
82  Gln Trp Asp Gly Ser His Ala Cys Gly Ala Thr Leu Ile Asn Ala Thr
83          210                 215                 220
85  tgg ctt gtg agt gct gct cac tgt ttt aca aca tat aag aac cct gcc        720
86  Trp Leu Val Ser Ala Ala His Cys Phe Thr Thr Tyr Lys Asn Pro Ala
87  225                 230                 235                 240
89  aga tgg act gct tcc ttt gga gta aca ata aaa cct tcg aaa atg aaa        768
90  Arg Trp Thr Ala Ser Phe Gly Val Thr Ile Lys Pro Ser Lys Met Lys
91              245                 250                 255
93  cgg ggt ctc cgg aga ata att gtc cat gaa aaa tac aaa cac cca tca        816
94  Arg Gly Leu Arg Arg Ile Ile Val His Glu Lys Tyr Lys His Pro Ser
95              260                 265                 270
97  cat gac tat gat att tct ctt gca gag ctt tct agc cct gtt ccc tac        864
98  His Asp Tyr Asp Ile Ser Leu Ala Glu Leu Ser Ser Pro Val Pro Tyr
99          275                 280                 285
101 aca aat gca gta cat aga gtt tgt ctc cct gat gca tcc tat gag ttt        912
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103     290                 295                 300
105 caa cca ggt gat gtg atg ttt gtg aca gga ttt gga gca ctg aaa aat        960
106 Gln Pro Gly Asp Val Met Phe Val Thr Gly Phe Gly Ala Leu Lys Asn
107 305                 310                 315                 320
109 gat ggt tac agt caa aat cat ctt cga caa gca cag gtg act ctc ata       1008
110 Asp Gly Tyr Ser Gln Asn His Leu Arg Gln Ala Gln Val Thr Leu Ile
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122 Gln Gly Asp Ser Gly Gly Pro Leu Val Ser Ser Asp Ala Arg Asp Ile
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126 Trp Tyr Leu Ala Gly Ile Val Ser Trp Gly Asp Glu Cys Ala Lys Pro
127 385                 390                 395                 400
129 aac aag cct ggt gtt tat act aga gtt acg gcc ttg cgg gac tgg att       1248
130 Asn Lys Pro Gly Val Tyr Thr Arg Val Thr Ala Leu Arg Asp Trp Ile
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154         35                  40                  45
157 Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr Thr Asp Lys Leu Tyr
158     50                  55                  60
161 Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn Phe Thr Glu Met Ser Gln
162 65                  70                  75                  80
165 Arg Leu Glu Ser Met Val Lys Asn Ala Phe Tyr Lys Ser Pro Leu Arg
166             85                  90                  95
169 Glu Glu Phe Val Lys Ser Gln Val Ile Lys Phe Ser Gln Asp Lys His
170             100                 105                 110
173 Gly Val Leu Ala His Met Leu Leu Ile Cys Arg Phe His Ser Thr Glu
174             115                 120                 125
177 Asp Pro Glu Thr Val Asp Lys Ile Val Gln Leu Val Leu His Glu Lys
178     130                 135                 140
181 Leu Gln Asp Ala Val Gly Pro Pro Lys Val Asp Pro His Ser Val Lys
182 145                 150                 155                 160
185 Ile Lys Lys Ile Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys
186             165                 170                 175
189 Cys Gly Thr Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val
190             180                 185                 190
193 Gly Gly Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu
194     195                 200                 205
197 Gln Trp Asp Gly Ser His Ala Cys Gly Ala Thr Leu Ile Asn Ala Thr
198     210                 215                 220
201 Trp Leu Val Ser Ala Ala His Cys Phe Thr Thr Tyr Lys Asn Pro Ala
202 225                 230                 235                 240
205 Arg Trp Thr Ala Ser Phe Gly Val Thr Ile Lys Pro Ser Lys Met Lys
206             245                 250                 255
209 Arg Gly Leu Arg Arg Ile Ile Val His Glu Lys Tyr Lys His Pro Ser
210             260                 265                 270
213 His Asp Tyr Asp Ile Ser Leu Ala Glu Leu Ser Ser Pro Val Pro Tyr
214     275                 280                 285
217 Thr Asn Ala Val His Arg Val Cys Leu Pro Asp Ala Ser Tyr Glu Phe
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222 305                 310                 315                 320
225 Asp Gly Tyr Ser Gln Asn His Leu Arg Gln Ala Gln Val Thr Leu Ile
226             325                 330                 335
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PATENT APPLICATION: US/09/674,035   TIME: 11:38:07

Input Set : A:\227274078.ST25.txt
Output Set: N:\CRF3\08312001\I674035.raw

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230         340                 345                 350
233 Pro Arg Ile Leu Cys Ala Gly Ser Leu Glu Gly Lys Thr Asp Ala Cys
234         355                 360                 365
237 Gln Gly Asp Ser Gly Gly Pro Leu Val Ser Ser Asp Ala Arg Asp Ile
238     370                 375                 380
241 Trp Tyr Leu Ala Gly Ile Val Ser Trp Gly Asp Glu Cys Ala Lys Pro
242 385                 390                 395                 400
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256 <213> ORGANISM: Homo sapiens
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268 Pro Trp Val Ile Gly Leu Val Met Phe Ile Ser Leu Ile Val Leu Ala
269             20                  25                  30
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272 Val Cys Ile Gly Val Thr Val His Tyr Val Arg Tyr Asn Gln Lys Lys
273             35                  40                  45
275 acc tac aat tac tat agc aca ttg tca ttt aca act gac aaa cta tat   192
276 Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr Thr Asp Lys Leu Tyr
277     50                  55                  60
279 gct gag ttt ggc aga gag gct tct aac aat ttt aca gaa atg agc cag   240
280 Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn Phe Thr Glu Met Ser Gln
281 65                  70                  75                  80
283 aga ctt gaa tca atg gtg aaa aat gca ttt tat aaa tct cca tta agg   288
284 Arg Leu Glu Ser Met Val Lys Asn Ala Phe Tyr Lys Ser Pro Leu Arg
285             85                  90                  95
287 gaa gaa ttt gtc aag tct cag gtt atc aag ttc agt caa cag aag cat   336
288 Glu Glu Phe Val Lys Ser Gln Val Ile Lys Phe Ser Gln Gln Lys His
289             100                 105                 110
291 gga gtg ttg gct cat atg ctg ttg att tct aga ttt cac tct act gag   384
292 Gly Val Leu Ala His Met Leu Leu Ile Ser Arg Phe His Ser Thr Glu
293             115                 120                 125
295 gat cct gaa act gta gat aaa att gtt caa ctt gtt tta cat gaa aag   432
296 Asp Pro Glu Thr Val Asp Lys Ile Val Gln Leu Val Leu His Glu Lys
297     130                 135                 140
299 ctg caa gat gct gta gga ccc cct aaa gta gat cct cac tca gtt aaa   480
300 Leu Gln Asp Ala Val Gly Pro Pro Lys Val Asp Pro His Ser Val Lys
```

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301 145                   150                   155                   160
303 att aaa aaa atc aac aag aca gaa aca gac agc tat cta aac cat tgc      528
304 Ile Lys Lys Ile Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys
305                   165                   170                   175
307 tgc gga aca cga aga agt aaa act cta ggt cag agt ctc agg atc gtt      576
308 Cys Gly Thr Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val
309                   180                   185                   190
311 ggt ggg aca gaa gta gaa gag ggt gaa tgg ccc tgg cag gct agc ctg      624
312 Gly Gly Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu
313              195                   200                   205
315 cag tgg gat ggg agt cat cgc tgt gga gca acc tta att aat gcc aca      672
316 Gln Trp Asp Gly Ser His Arg Cys Gly Ala Thr Leu Ile Asn Ala Thr
317      210                   215                   220
319 tgg ctt gtg agt gct gct cac tgt ttt aca aca tat aag aac cct gcc      720
320 Trp Leu Val Ser Ala Ala His Cys Phe Thr Thr Tyr Lys Asn Pro Ala
321 225                   230                   235                   240
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324 Arg Trp Thr Ala Ser Phe Gly Val Thr Ile Lys Pro Ser Lys Met Lys
325                   245                   250                   255
327 cgg ggt ctc cgg aga ata att gtc cat gaa aaa tac aaa cac cca tca      816
328 Arg Gly Leu Arg Arg Ile Ile Val His Glu Lys Tyr Lys His Pro Ser
329              260                   265                   270
331 cat gac tat gat att tct ctt gca gag ctt tct agc cct gtt ccc tac      864
332 His Asp Tyr Asp Ile Ser Leu Ala Glu Leu Ser Ser Pro Val Pro Tyr
333         275                   280                   285
335 aca aat gca gta cat aga gtt tgt ctc cct gat gca tcc tat gag ttt      912
336 Thr Asn Ala Val His Arg Val Cys Leu Pro Asp Ala Ser Tyr Glu Phe
337      290                   295                   300
339 caa cca ggt gat gtg atg ttt gtg aca gga ttt gga gca ctg aaa aat      960
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343 gat ggt tac agt caa aat cat ctt cga caa gca cag gtg act ctc ata     1008
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355 cag ggt gac tct gga gga cca ctg gtt agt tca gat gct aga gat atc     1152
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361 385                   390                   395                   400
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364 Asn Lys Pro Gly Val Tyr Thr Arg Val Thr Ala Leu Arg Asp Trp Ile
365                   405                   410                   415
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VERIFICATION SUMMARY   DATE: 08/31/2001
PATENT APPLICATION: **US/09/674,035**   TIME: 11:38:09

Input Set : **A:\227274078.ST25.txt**
Output Set: **N:\CRF3\08312001\I674035.raw**

STATISTICS SUMMARY   DATE: 08/31/2001
PATENT APPLICATION: **US/09/674,035**   TIME: 11:38:09

Input Set : **A:\227274078.ST25.txt**
Output Set: **N:\CRF3\08312001\I674035.raw**

Application Serial Number: US/09/674,035
Alpha or Numeric: Numeric
Application Class:
Application File Date: 11-11-1999
Art Unit: PCT
Software Application: PatentIn
Total Number of Sequences: 10
Total Nucleotides: 2696
Total Amino Acids: 844
Number of Errors: 0
Number of Warnings: 0
Number of Corrections: 0

MESSAGE SUMMARY